

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

(i) APPLICANT: BAICHWAL, VIJAY R  
HUANG, JIANING  
HSU, HAILING  
GOEDDEL, DAVID V

10 (ii) TITLE OF INVENTION: RIP: NOVEL HUMAN PROTEIN INVOLVED IN  
TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING  
ASSAYS

15 (iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
(B) STREET: 75 DENISE DRIVE  
(C) CITY: HILLSBOROUGH  
20 (D) STATE: CALIFORNIA  
(E) COUNTRY: USA  
(F) ZIP: 94010

25 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
30 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
25 (B) FILING DATE:  
(C) CLASSIFICATION:

30 (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: OSMAN, RICHARD A.  
(B) REGISTRATION NUMBER: 36,627  
35 (C) REFERENCE/DOCKET NUMBER: T95-006-1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650) 343-4341  
40 (B) TELEFAX: (650) 343-4342

35 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2016 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
45 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
40 (B) LOCATION: 1..2013

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG	CAA	CCA	GAC	ATG	TCC	TTG	AAT	GTC	ATT	AAG	ATG	AAA	TCC	AGT	GAT	48		
Met	Gln	Pro	Asp	Met	Ser	Leu	Asn	Val	Ile	Lys	Met	Lys	Ser	Ser	Asp			
1	5	10	15															
5	TTC	CTG	GAG	AGT	GCA	GAA	CTG	GAC	AGC	GGA	GGC	TTT	GGG	AAG	CTG	TCT	96	
	Phe	Leu	Glu	Ser	Ala	Glu	Leu	Asp	Ser	Gly	Gly	Phe	Gly	Lys	Val	Ser		
	20	25	30															
10	CTG	TGT	TTC	CAC	AGA	ACC	CAG	GGA	CTG	ATG	ATC	ATG	AAA	ACA	GTG	TAC	144	
	Leu	Cys	Phe	His	Arg	Thr	Gln	Gly	Leu	Met	Ile	Met	Lys	Thr	Val	Tyr		
	35	40	45															
15	AAG	GGG	CCC	AAC	TGC	ATT	GAG	CAC	AAE	GAG	GCC	CTC	TTG	GAG	GAG	GCG	192	
	Lys	Gly	Pro	Asn	Cys	Ile	Glu	His	Asn	Glu	Ala	Leu	Leu	Glu	Glu	Ala		
	50	55	60															
20	AAG	ATG	ATG	AAC	AGA	CTG	AGA	CAC	AGC	CGG	GTG	GTG	AAG	CTC	CTG	GGC	240	
	Lys	Met	Met	Asn	Arg	Leu	Arg	His	Ser	Arg	Val	Val	Lys	Leu	Leu	Gly		
	65	70	75															
25	GTC	ATC	ATA	GAG	GAA	GGG	AAG	TAC	TCC	CTG	GTG	ATG	GAG	TAC	ATG	GAG	288	
	Val	Ile	Ile	Glu	Glu	Gly	Lys	Tyr	Ser	Leu	Val	Met	Glu	Tyr	Met	Glu		
	85	90	95															
30	AAG	GGC	AAC	CTG	ATG	CAC	GTG	CTG	AAA	GCC	GAG	ATG	AGT	ACT	CCG	CTT	336	
	Lys	Gly	Asn	Leu	Met	His	Val	Leu	Lys	Ala	Glu	Met	Ser	Thr	Pro	Leu		
	100	105	110															
35	TCT	GTA	AAA	GGA	AGG	ATA	ATT	TTG	GAA	ATC	ATT	GAA	GGA	ATG	TGC	TAC	384	
	Ser	Val	Lys	Gly	Arg	Ile	Ile	Leu	Glu	Ile	Ile	Glu	Gly	Met	Cys	Tyr		
	115	120	125															
40	TTA	CAT	GGA	AAA	GGC	GTG	ATA	CAC	AAG	GAC	CTG	AAG	CCT	GAA	AAT	ATC	432	
	Leu	His	Gly	Lys	Gly	Val	Ile	His	Lys	Ile	Ala	Asp	Leu	Lys	Pro	Glu	Asn	Ile
	130	135	140															
45	CTT	GTT	GAT	AAT	GAC	TTC	CAC	ATT	AAG	ATC	GCA	GAC	CTC	GGC	CTT	GCC	480	
	Leu	Val	Asp	Asn	Asp	Phe	His	Ile	Lys	Ile	Ala	Asp	Leu	Gly	Leu	Ala		
	145	150	155															
50	TCC	TTT	AAG	ATG	TGG	AGC	AAA	CTG	AAT	AAT	GAA	GAG	CAC	AAT	GAG	CTG	523	
	Ser	Phe	Lys	Met	Trp	Ser	Lys	Leu	Asn	Asn	Glu	Glu	His	Asn	Glu	Leu		
	165	170	175															
55	AGG	GAA	GTG	GAC	GGC	ACC	GCT	AAG	AAG	AAT	GGC	GGC	ACC	CTC	TAC	TAC	576	
	Arg	Glu	Val	Asp	Gly	Thr	Ala	Lys	Lys	Asn	Gly	Gly	Thr	Leu	Tyr	Tyr		
	180	185	190															
60	ATG	CGC	CCC	GAG	CAC	CTG	AAT	GAC	GTC	AAC	GCA	AAG	CCC	ACA	GAG	AAG	624	
	Met	Ala	Pro	Glu	His	Leu	Asn	Asp	Val	Asn	Ala	Lys	Pro	Thr	Glu	Lys		
	195	200	205															
65	TCG	GAT	GTG	TAC	AGC	TTT	GCT	GTA	GTC	CTC	TGG	GCG	ATA	TTT	GCA	AAT	672	
	Ser	Asp	Val	Tyr	Ser	Phe	Ala	Val	Leu	Trp	Ala	Ile	Phe	Ala	Asn			
	210	215	220															
70	AAG	GAG	CCA	TAT	GAA	AAT	GCT	ATC	TGT	GAG	CAG	CAG	TTG	ATA	ATG	TGC	720	

Lys	Glu	Pro	Tyr	Glu	Asn	Ala	Ile	Cys	Glu	Gln	Gln	Leu	Ile	Met	Cys		
225				230					235					240			
ATA	AAA	TCT	GGG	AAC	AGG	CCA	GAT	GTG	GAT	GAC	ATC	ACT	GAG	TAC	TGC	768	
Ile	Lys	Ser	Gly	Asn	Arg	Pro	Asp	Val	Asp	Asp	Ile	Thr	Glu	Tyr	Cys		
5				245					250				255				
CCA	AGA	GAA	ATT	ATC	AGT	CTC	ATG	AAG	CTC	TGC	TGG	GAA	GCG	AAT	CGG	816	
Pro	Arg	Glu	Ile	Ile	Ser	Leu	Met	Lys	Leu	Cys	Trp	Glu	Ala	Asn	Pro		
			260					265			270						
GAA	GCT	CGG	CCG	ACA	TTT	CCT	GGC	ATT	GAA	GAA	AAA	TTT	AGG	CCT	TTT	864	
10	Glu	Ala	Arg	Pro	Thr	Phe	Pro	Gly	Ile	Glu	Glu	Lys	Phe	Arg	Pro	Phe	
	275			280					285								
TAT	TTA	AGT	CAA	TTA	GAA	GAA	AGT	GTA	GAA	GAG	GAC	GTG	AAG	AGT	TTA	912	
Tyr	Leu	Ser	Gln	Leu	Glu	Glu	Ser	Val	Glu	Glu	Asp	Val	Lys	Ser	Leu		
	290			295				300									
15	AAG	AAA	GAG	TAT	TCA	AAC	GAA	AAT	GCA	GTT	GTG	AAG	AGA	ATG	CAG	TCT	960
Lys	Lys	Glu	Tyr	Ser	Asn	Glu	Asn	Ala	Val	Val	Lys	Arg	Met	Gln	Ser		
	305			310				315			320						
CTT	CAA	CTT	GAT	TGT	GTG	GCA	GTA	CCT	TCA	AGC	CGG	TCA	AAT	TCA	GCC	1008	
Leu	Gln	Leu	Asp	Cys	Val	Ala	Val	Pro	Ser	Ser	Arg	Ser	Asn	Ser	Ala		
20				325				330			335						
ACA	GAA	CAG	CCT	GGT	TCA	CTG	CAC	AGT	TCC	CAG	GGA	CTT	GGG	ATG	GGT	1056	
Thr	Glu	Gln	Pro	Gly	Ser	Leu	His	Ser	Ser	Gln	Gly	Leu	Gly	Met	Gly		
	340			345				350									
CCT	GTG	GAG	GAG	TCC	TGG	TTT	GCT	CCT	TCC	CTG	GAG	CAC	CCA	CAA	GAA	1104	
25	Pro	Val	Glu	Glu	Ser	Trp	Phe	Ala	Pro	Ser	Leu	Glu	His	Pro	Gln	Glu	
	355			360				365									
GAG	AAT	GAG	CCC	AGC	CTG	CAG	AGT	AAA	CTC	CAA	GAC	GAA	GCC	AAC	TAC	1152	
Glu	Asn	Glu	Pro	Ser	Leu	Gln	Ser	Lys	Leu	Gln	Asp	Glu	Ala	Asn	Tyr		
	370			375				380									
30	CAT	CTT	TAT	GGC	AGC	CGC	ATG	GAC	AGG	CAG	ACG	AAA	CAG	CAG	CCC	AGA	1200
His	Leu	Tyr	Gly	Ser	Arg	Met	Asp	Arg	Gln	Thr	Lys	Gln	Gln	Pro	Arg		
	385			390				395			400						
CAG	AAT	GTG	GCT	TAC	AAC	AGA	GAG	GAG	GAA	AGG	AGA	CGC	AGG	GTC	TCC	1248	
Gln	Asn	Val	Ala	Tyr	Asn	Arg	Glu	Glu	Glu	Arg	Arg	Arg	Arg	Arg	Val	Ser	
35				405				410			415						
CAT	GAC	CCT	TTT	GCA	CAG	CAA	AGA	CCT	TAC	GAG	AAT	TTT	CAG	AAT	ACA	1296	
His	Asp	Pro	Phe	Ala	Gln	Gln	Arg	Pro	Tyr	Glu	Asn	Phe	Gln	Asn	Thr		
	420			425				430									
GAG	GGA	AAA	GGC	ACT	GTT	TAT	TCC	AGT	GCA	GCC	AGT	CAT	GGT	AAT	GCA	1344	
40	Glu	Gly	Lys	Gly	Thr	Val	Tyr	Ser	Ser	Ala	Ala	Ser	His	Gly	Asn	Ala	
	435			440				445									
GTG	CAC	CAG	CCC	TCA	GGG	CTC	ACC	AGC	CAA	CCT	CAA	GTA	CTG	TAT	CAG	1392	
Val	His	Gln	Pro	Ser	Gly	Leu	Thr	Ser	Gln	Pro	Gln	Val	Leu	Tyr	Gln		
	450			455				460									

AAC AAT GGA TTA TAT AGC TCA CAT GGC TTT GGA ACA AGA CCA CTG GAT	1440
Asn Asn Gly Leu Tyr Ser Ser His Gly Phe Gly Thr Arg Pro Leu Asp	
465 470 475 480	
CCA GGA ACA GCA GGT CCC AGA GTT TGG TAC AGG CCA ATT CCA AGT CAT	1488
5 Pro Gly Thr Ala Gly Pro Arg Val Trp Tyr Arg Pro Ile Pro Ser His	
485 490 495	
ATG CCT AGT CTG CAT AAT ATC CCA GTG CCT GAG ACC AAC TAT CTA GGA	1536
Met Pro Ser Leu His Asn Ile Pro Val Pro Glu Thr Asn Tyr Leu Gly	
500 505 510	
10 AAT ACA CCC ACC ATG CCA TTC AGC TCC TTG CCA CCA ACA GAT GAA TCT	1584
Asn Thr Pro Thr Met Pro Phe Ser Ser Leu Pro Pro Thr Asp Glu Ser	
515 520 525	
ATA AAA TAT ACC ATA TAC AAT AGT ACT GGC ATT CAG ATT GGA GCC TAC	1632
Ile Lys Tyr Thr Ile Tyr Asn Ser Thr Gly Ile Gln Ile Gly Ala Tyr	
15 530 535 540	
AAT TAT ATG GAG ATT GGT GGG ACG AGT TCA TCA CTA CTA GAC AGC ACA	1680
Asn Tyr Met Glu Ile Gly Gly Thr Ser Ser Ser Leu Leu Asp Ser Thr	
545 550 555 560	
AAT ACG AAC TTC AAA GAA GAG CCA GCT GCT AAG TAC CAA GCT ATC TTT	1728
20 Asn Thr Asn Phe Lys Glu Glu Pro Ala Ala Lys Tyr Gln Ala Ile Phe	
565 570 575	
GAT AAT ACC ACT AGT CTG ACG GAT AAA CAC CTG GAC CCA ATC AGG GAA	1776
Asp Asn Thr Thr Ser Leu Thr Asp Lys His Leu Asp Pro Ile Arg Glu	
580 585 590	
25 AAT CTG GGA AAG CAC TGG AAA AAC TGT GCC CGT AAA CTG GGC TTC ACA	1824
Asn Leu Gly Lys His Trp Lys Asn Cys Ala Arg Lys Leu Gly Phe Thr	
595 600 605	
CAG TCT CAG ATT GAT GAA ATT GAC CAT GAC TAT GAG CGA GAT GGA CTG	1872
Gln Ser Gln Ile Asp Glu Ile Asp His Asp Tyr Glu Arg Asp Gly Leu	
30 610 615 620	
AAA GAA AAG GTT TAC CAG ATG CTC CAA AAG TGG GTG ATG AGG GAA GGC	1920
Lys Glu Lys Val Tyr Gln Met Leu Gln Lys Trp Val Met Arg Glu Gly	
625 630 635 640	
ATA AAG GGA GCC ACG GTG GGG AAG CTG GCC CAG GCG CTC CAC CAG TGT	1968
35 Ile Lys Gly Ala Thr Val Gly Lys Leu Ala Gln Ala Leu His Gln Cys	
645 650 655	
TCC AGG ATC GAC CTT CTG AGC AGC TTG ATT TAC GTC AGC CAG AAC	2013
Ser Arg Ile Asp Leu Leu Ser Ser Leu Ile Tyr Val Ser Gln Asn	
660 665 670	
40 TAA	2016

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 671 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

5 Met Gln Pro Asp Met Ser Leu Asn Val Ile Lys Met Lys Ser Ser Asp  
1 5 10 15  
Phe Leu Glu Ser Ala Glu Leu Asp Ser Gly Gly Phe Gly Lys Val Ser  
20 25 30  
Leu Cys Phe His Arg Thr Gln Gly Leu Met Ile Met Lys Thr Val Tyr  
10 35 40 45  
Lys Gly Pro Asn Cys Ile Glu His Asn Glu Ala Leu Leu Glu Glu Ala  
50 55 60  
Lys Met Met Asn Arg Leu Arg His Ser Arg Val Val Lys Leu Leu Gly  
65 70 75 80  
15 Val Ile Ile Glu Glu Gly Lys Tyr Ser Leu Val Met Glu Tyr Met Glu  
85 90 95  
Lys Gly Asn Leu Met His Val Leu Lys Ala Glu Met Ser Thr Pro Leu  
100 105 110  
Ser Val Lys Gly Arg Ile Ile Leu Glu Ile Ile Glu Gly Met Cys Tyr  
20 115 120 125  
Leu His Gly Lys Gly Val Ile His Lys Asp Leu Lys Pro Glu Asn Ile  
130 135 140  
Leu Val Asp Asn Asp Phe His Ile Lys Ile Ala Asp Leu Gly Leu Ala  
145 150 155 160  
25 Ser Phe Lys Met Trp Ser Lys Leu Asn Asn Glu Glu His Asn Glu Leu  
165 170 175  
Arg Glu Val Asp Gly Thr Ala Lys Lys Asn Gly Gly Thr Leu Tyr Tyr  
180 185 190  
Met Ala Pro Glu His Leu Asn Asp Val Asn Ala Lys Pro Thr Glu Lys  
30 195 200 205  
Ser Asp Val Tyr Ser Phe Ala Val Val Leu Trp Ala Ile Phe Ala Asn  
210 215 220  
Lys Glu Pro Tyr Glu Asn Ala Ile Cys Glu Gln Gln Leu Ile Met Cys  
225 230 235 240  
35 Ile Lys Ser Gly Asn Arg Pro Asp Val Asp Asp Ile Thr Glu Tyr Cys  
245 250 255  
Pro Arg Glu Ile Ile Ser Leu Met Lys Leu Cys Trp Glu Ala Asn Pro  
260 265 270  
Glu Ala Arg Pro Thr Phe Pro Gly Ile Glu Glu Lys Phe Arg Pro Phe  
40 275 280 285  
Tyr Leu Ser Gln Leu Glu Glu Ser Val Glu Glu Asp Val Lys Ser Leu  
290 295 300  
Lys Lys Glu Tyr Ser Asn Glu Asn Ala Val Val Lys Arg Met Gln Ser  
305 310 315 320

Leu Gln Leu Asp Cys Val Ala Val Pro Ser Ser Arg Ser Asn Ser Ala			
325	330	335	
Thr Glu Gln Pro Gly Ser Leu His Ser Ser Gln Gly Leu Gly Met Gly			
340	345	350	
5 Pro Val Glu Glu Ser Trp Phe Ala Pro Ser Leu Glu His Pro Gln Glu			
355	360	365	
Glu Asn Glu Pro Ser Leu Gln Ser Lys Leu Gln Asp Glu Ala Asn Tyr			
370	375	380	
His Leu Tyr Gly Ser Arg Met Asp Arg Gln Thr Lys Gln Gln Pro Arg			
10 385	390	395	400
Gln Asn Val Ala Tyr Asn Arg Glu Glu Arg Arg Arg Arg Val Ser			
405	410	415	
His Asp Pro Phe Ala Gln Gln Arg Pro Tyr Glu Asn Phe Gln Asn Thr			
420	425	430	
15 Glu Gly Lys Gly Thr Val Tyr Ser Ser Ala Ala Ser His Gly Asn Ala			
435	440	445	
Val His Gln Pro Ser Gly Leu Thr Ser Gln Pro Gln Val Leu Tyr Gln			
450	455	460	
Asn Asn Gly Leu Tyr Ser Ser His Gly Phe Gly Thr Arg Pro Leu Asp			
20 465	470	475	480
Pro Gly Thr Ala Gly Pro Arg Val Trp Tyr Arg Pro Ile Pro Ser His			
485	490	495	
Met Pro Ser Leu His Asn Ile Pro Val Pro Glu Thr Asn Tyr Leu Gly			
500	505	510	
25 Asn Thr Pro Thr Met Pro Phe Ser Ser Leu Pro Pro Thr Asp Glu Ser			
515	520	525	
Ile Lys Tyr Thr Ile Tyr Asn Ser Thr Gly Ile Gln Ile Gly Ala Tyr			
530	535	540	
Asn Tyr Met Glu Ile Gly Thr Ser Ser Ser Leu Leu Asp Ser Thr			
30 545	550	555	560
Asn Thr Asn Phe Lys Glu Glu Pro Ala Ala Lys Tyr Gln Ala Ile Phe			
565	570	575	
Asp Asn Thr Thr Ser Leu Thr Asp Lys His Leu Asp Pro Ile Arg Glu			
580	585	590	
35 Asn Leu Gly Lys His Trp Lys Asn Cys Ala Arg Lys Leu Gly Phe Thr			
595	600	605	
Gln Ser Gln Ile Asp Glu Ile Asp His Asp Tyr Glu Arg Asp Gly Leu			
610	615	620	
Lys Glu Lys Val Tyr Gln Met Leu Gln Lys Trp Val Met Arg Glu Gly			
40 625	630	635	640
Ile Lys Gly Ala Thr Val Gly Lys Leu Ala Gln Ala Leu His Gln Cys			
645	650	655	
Ser Arg Ile Asp Leu Leu Ser Ser Leu Ile Tyr Val Ser Gln Asn			
660	665	670	